

096,006D - SeqList.ST25.txt  
SEQUENCE LISTING

<110> Geron Corporation

McWhir, Jim

Gold, Joseph D.

Schiff, J. Michael

<120> Selective Antibody Targeting of Undifferentiated Stem Cells

<130> 096,006D- SeqList

<140> to be assigned

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<150> 09/995,419

<151> 2001-11-26

<150> 60/253,357

<151> 2000-11-27

<150> 60/253,443

<151> 2000-11-27

<150> 60/253,395

<151> 2000-11-27

<160> 20

<170> PatentIn version 3.1

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## 096,006D - SeqList.ST25.txt

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Asp	Glu	Ser	His	Leu	Asn	Lys	Tyr	Phe	Leu	Leu	Asn	Lys	Pro	Thr	Lys	
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Arg Val Ile Phe Tyr Val Met Val Asp Asp Val Ser Arg Met Pro Leu  
Page 13

165

170

175

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Glu Cys Phe Lys Gly Ile Leu Leu Asp Lys Lys Asn Asp Ile Glu Ala  
 305 310 315 320

Glu Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu Leu Asn Lys  
 325 330 335

Pro Ser Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr His Ile Gly  
 340 345 350

Leu Pro Ser Asp Ile Lys Thr Val Lys Leu Ser Trp Gln Thr Lys Glu  
 355 360 365

Tyr Asn Leu Val Arg Lys Asn Val  
 370 375

<210> 10  
 <211> 1062  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1062)  
 <223>

<400> 10  
 atg gcc gag gtg ttg cgg acg ctg gcc gga aaa cca aaa tgc cac gca 48  
 Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala  
 1 5 10 15

ctt cga cct atg atc ctt ttc cta ata atg ctt gtc ttg gtc ttg ttt 96  
 Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe  
 20 25 30

ggt tac ggg gtc cta agc ccc aga agt cta atg cca gga agc ctg gaa 144  
 Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu  
 35 40 45

cgg ggg ttc tgc atg gct gtt agg gaa cct gac cat ctg cag cgc gtc 192  
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Arg	Gly	Phe	Cys	Met	Ala	Val	Arg	Glu	Pro	Asp	His	Leu	Gln	Arg	Val	
50						55				60						
tcg	ttg	cca	agg	atg	gtc	tac	ccc	cag	cca	aag	gtg	ctg	aca	ccg	tgg	240
Ser	Leu	Pro	Arg	Met	Val	Tyr	Pro	Gln	Pro	Lys	Val	Leu	Thr	Pro	Trp	
65					70					75					80	
aag	gat	gtc	ctc	gtg	gtg	acc	cct	tgg	ctg	gct	ccc	att	gtc	tgg	gag	288
Lys	Asp	Val	Leu	Val	Val	Thr	Pro	Trp	Leu	Ala	Pro	Ile	Val	Trp	Glu	
				85					90					95		
ggc	aca	ttc	aac	atc	gac	atc	ctc	aac	gag	cag	ttc	agg	ctc	cag	aac	336
Gly	Thr	Phe	Asn	Ile	Asp	Ile	Leu	Asn	Glu	Gln	Phe	Arg	Leu	Gln	Asn	
			100					105					110			
acc	acc	att	ggg	tta	act	gtg	ttt	gcc	atc	aag	aaa	tac	gtg	gct	ttc	384
Thr	Thr	Ile	Gly	Leu	Thr	Val	Phe	Ala	Ile	Lys	Lys	Tyr	Val	Ala	Phe	
		115					120					125				
ctg	aag	ctg	ttc	ctg	gag	acg	gcg	gag	aag	cac	ttc	atg	gtg	ggc	cac	432
Leu	Lys	Leu	Phe	Leu	Glu	Thr	Ala	Glu	Lys	His	Phe	Met	Val	Gly	His	
	130					135					140					
cgt	gtc	cac	tac	tat	gtc	ttc	acc	gac	cag	ctg	gcc	gcg	gtg	ccc	cgc	480
Arg	Val	His	Tyr	Tyr	Val	Phe	Thr	Asp	Gln	Leu	Ala	Ala	Val	Pro	Arg	
145					150					155					160	
gtg	acg	ctg	ggg	acc	ggt	cgg	cag	ctg	tca	gtg	ctg	gag	gtg	cgc	gcc	528
Val	Thr	Leu	Gly	Thr	Gly	Arg	Gln	Leu	Ser	Val	Leu	Glu	Val	Arg	Ala	
				165					170					175		
tac	aag	cgc	tgg	cag	gac	gtg	tcc	atg	cgc	cgc	atg	gag	atg	atc	agt	576
Tyr	Lys	Arg	Trp	Gln	Asp	Val	Ser	Met	Arg	Arg	Met	Glu	Met	Ile	Ser	
			180					185					190			
gac	ttc	tgc	gag	cgg	cgc	ttc	ctc	agc	gag	gtg	gat	tac	ctg	gtg	tgc	624
Asp	Phe	Cys	Glu	Arg	Arg	Phe	Leu	Ser	Glu	Val	Asp	Tyr	Leu	Val	Cys	
		195					200					205				
gtg	gac	gtg	gac	atg	gag	ttc	cgc	gac	cac	gtg	ggc	gtg	gag	atc	ctg	672
Val	Asp	Val	Asp	Met	Glu	Phe	Arg	Asp	His	Val	Gly	Val	Glu	Ile	Leu	
	210					215					220					
act	ccg	ctg	ttc	ggc	acc	ctg	cac	ccc	ggc	ttc	tac	gga	agc	agc	cgg	720
Thr	Pro	Leu	Phe	Gly	Thr	Leu	His	Pro	Gly	Phe	Tyr	Gly	Ser	Ser	Arg	
225					230				235						240	
gag	gcc	ttc	acc	tac	gag	cgc	cgg	ccc	cag	tcc	cag	gcc	tac	atc	ccc	768
Glu	Ala	Phe	Thr	Tyr	Glu	Arg	Arg	Pro	Gln	Ser	Gln	Ala	Tyr	Ile	Pro	
				245					250					255		
aag	gac	gag	ggc	gat	ttc	tac	tac	ctg	ggg	ggg	ttc	ttc	ggg	ggg	tcg	816
Lys	Asp	Glu	Gly	Asp	Phe	Tyr	Tyr	Leu	Gly	Gly	Phe	Phe	Gly	Gly	Ser	
			260					265					270			
gtg	caa	gag	gtg	cag	cgg	ctc	acc	agg	gcc	tgc	cac	cag	gcc	atg	atg	864
Val	Gln	Glu	Val	Gln	Arg	Leu	Thr	Arg	Ala	Cys	His	Gln	Ala	Met	Met	
			275				280					285				
gtc	gac	cag	gcc	aac	ggc	atc	gag	gcc	gtg	tgg	cac	gac	gag	agc	cac	912
Val	Asp	Gln	Ala	Asn	Gly	Ile	Glu	Ala	Val	Trp	His	Asp	Glu	Ser	His	
	290					295					300					

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ctg aac aag tac ctg ctg cgc cac aaa ccc acc aag gtg ctc tcc ccc	960
Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser Pro	
305 310 315 320	
gag tac ttg tgg gac cag cag ctg ctg ggc tgg ccc gcc gtc ctg agg	1008
Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu Arg	
325 330 335	
aag ctg agg ttc act gcg gtg ccc aag aac cac cag gcg gtc cgg aac	1056
Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg Asn	
340 345 350	
ccg tga	1062
Pro	

<210> 11

<211> 353

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala	
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Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe	
20 25 30	
Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu	
35 40 45	
Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val	
50 55 60	
Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Trp	
65 70 75 80	
Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp Glu	
85 90 95	
Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln Asn	
100 105 110	
Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala Phe	
115 120 125	
Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly His	
130 135 140	

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Arg Val His Tyr Tyr Val Phe Thr Asp Gln Leu Ala Ala Val Pro Arg  
145 150 155 160

Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Arg Ala  
165 170 175

Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile Ser  
180 185 190

Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val Cys  
195 200 205

Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile Leu  
210 215 220

Thr Pro Leu Phe Gly Thr Leu His Pro Gly Phe Tyr Gly Ser Ser Arg  
225 230 235 240

Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile Pro  
245 250 255

Lys Asp Glu Gly Asp Phe Tyr Tyr Leu Gly Gly Phe Phe Gly Gly Ser  
260 265 270

Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met Met  
275 280 285

Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser His  
290 295 300

Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser Pro  
305 310 315 320

Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu Arg  
325 330 335

Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg Asn  
340 345 350

Pro

<210> 12

<211> 1065

<212> DNA

096,006D - SeqList.ST25.txt

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1065)

<223>

<400> 12

atg gcc gag gtg ttg cgg acg ctg gcc gga aaa cca aaa tgc cac gca	48
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ctt cga cct atg atc ctt ttc cta ata atg ctt gtc ttg gtc ttg ttt	96
Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe	
20 25 30	
ggt tac ggg gtc cta agc ccc aga agt cta atg cca gga agc ctg gaa	144
Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu	
35 40 45	
cgg ggg ttc tgc atg gct gtt agg gaa cct gac cat ctg cag cgc gtc	192
Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val	
50 55 60	
tcg ttg cca agg atg gtc tac ccc cag cca aag gtg ctg aca ccg tgt	240
Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Cys	
65 70 75 80	
agg aag gat gtc ctc gtg gtg acc cct tgg ctg gct ccc att gtc tgg	288
Arg Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp	
85 90 95	
gag ggc acg ttc aac atc gac atc ctc aac gag cag ttc agg ctc cag	336
Glu Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln	
100 105 110	
aac acc acc att ggg tta act gtg ttt gcc atc aag aaa tac gtg gct	384
Asn Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala	
115 120 125	
ttc ctg aag ctg ttc ctg gag acg gcg gag aag cac ttc atg gtg ggc	432
Phe Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly	
130 135 140	
cac cgt gtc cac tac tat gtc ttc acc gac cag ccg gcc gcg gtg ccc	480
His Arg Val His Tyr Val Phe Thr Asp Gln Pro Ala Ala Val Pro	
145 150 155 160	
cgc gtg acg ctg ggg acc ggt cgg cag ctg tca gtg ctg gag gtg ggc	528
Arg Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Gly	
165 170 175	
gcc tac aag cgc tgg cag gac gtg tcc atg cgc cgc atg gag atg atc	576
Ala Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile	
180 185 190	

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agt gac ttc tgc gag cgg cgc ttc ctc agc gag gtg gat tac ctg gtg Ser Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val	624
195 200 205	
tgc gtg gac gtg gac atg gag ttc cgc gac cat gtg ggc gtg gag atc Cys Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile	672
210 215 220	
ctg act ccg ctg ttc ggc acc ctg cac ccc agc ttc tac gga agc agc Leu Thr Pro Leu Phe Gly Thr Leu His Pro Ser Phe Tyr Gly Ser Ser	720
225 230 235 240	
cgg gag gcc ttc acc tac gag cgc cgg ccc cag tcc cag gcc tac atc Arg Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile	768
245 250 255	
ccc aag gac gag ggc gat ttc tac tac atg ggg gcg ttc ttc ggg ggg Pro Lys Asp Glu Gly Asp Phe Tyr Tyr Met Gly Ala Phe Phe Gly Gly	816
260 265 270	
tcg gtg caa gag gtg cag cgg ctc acc agg gcc tgc cac cag gcc atg Ser Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met	864
275 280 285	
atg gtc gac cag gcc aac ggc atc gag gcc gtg tgg cac gac gag agc Met Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser	912
290 295 300	
cac ctg aac aag tac cta ctg cgc cac aaa ccc acc aag gtg ctc tcc His Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser	960
305 310 315 320	
ccc gag tac ttg tgg gac cag cag ctg ctg ggc tgg ccc gcc gtc ctg Pro Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu	1008
325 330 335	
agg aag ctg agg ttc act gcg gtg ccc aag aac cac cag gcg gtc cgg Arg Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg	1056
340 345 350	
aac ccg tga Asn Pro	1065

<210> 13

<211> 354

<212> PRT

<213> Homo sapiens

<400> 13

Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala  
1 5 10 15

Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe  
Page 23

Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu  
35 40 45

Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val  
50 55 60

Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Cys  
65 70 75 80

Arg Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp  
85 90 95

Glu Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln  
100 105 110

Asn Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala  
115 120 125

Phe Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly  
130 135 140

His Arg Val His Tyr Tyr Val Phe Thr Asp Gln Pro Ala Ala Val Pro  
145 150 155 160

Arg Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Gly  
165 170 175

Ala Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile  
180 185 190

Ser Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val  
195 200 205

Cys Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile  
210 215 220

Leu Thr Pro Leu Phe Gly Thr Leu His Pro Ser Phe Tyr Gly Ser Ser  
225 230 235 240

Arg Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile  
245 250 255

Pro Lys Asp Glu Gly Asp Phe Tyr Tyr Met Gly Ala Phe Phe Gly Gly  
260 265 270

Ser Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met  
275 280 285

Met Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser  
290 295 300

His Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser  
305 310 315 320

Pro Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu  
325 330 335

Arg Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg  
340 345 350

Asn Pro

<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Amplification Primer

<220>

<221> misc\_feature

<222> (1)..(23)

<223> Amplification Primer

<400> 14

ggcctgtact acatttgccct gga

23

<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Amplification Primer

<220>

<221> misc\_feature

<222> (1)..(26)

<223> Amplification Primer

<400> 15  
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26

<210> 16

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Amplification Primer

<220>

<221> misc\_feature

<222> (1)..(55)

<223> Amplification Primer

<400> 16  
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55

<210> 17

<211> 50

<212> PRT

<213> Mus musculus

<400> 17

Met Ile Thr Met Leu Gln Asp Leu His Val Asn Lys Ile Ser Met Ser  
1 5 10 15

Arg Ser Lys Ser Glu Thr Ser Leu Pro Ser Ser Arg Ser Gly Ser Gln  
20 25 30

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Glu Lys Ile Met Asn Val Lys Gly Lys Val Ile Leu Leu Met Leu Ile  
 35 40 45

Val Ser  
 50

<210> 18

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimera Mouse/Pig

<400> 18

Met Trp Leu Arg Ser His Arg Gln Val Ile Leu Leu Met Leu Ile Val  
 1 5 10 15

Ser

<210> 19

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimera Mouse/Pig

<400> 19

Met Trp Leu Arg Ser His Arg Gln Val Val Leu Ser Met Leu Leu Val  
 1 5 10 15

Ser

<210> 20

<211> 15

<212> PRT

096,006D - SeqList.ST25.txt

<213> Sus scrofa

<400> 20

Met	Asn	Val	Lys	Gly	Arg	Val	Val	Leu	Ser	Met	Leu	Leu	Val	Ser
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